Figure 1A

	1	DIVLTQSPAS	LAVSLGQRAT	MSCRAGESVD	IFGVGFLHWY	QQKPGQPPKL
	51	LIYRASNLES	GIPVRFSGTG	sRTDFTLIID	PVEADDVATY	YCQQTNEDPY
_						
	101	TFGGGTKLEI	KGGGGSGGG	SGGGGSGGG	SGGGGSGGG	SEVQLQQSGA
_						
	151	ELVEPGASVK	LSCTASGFNI	KDTYMHWVKQ	RPEQGLEWIG	RIDPANGNSK
			•			
	201	YVPKFQGKAT	ITADTSSNTA	YLQLTSLTSE	DTAVYYCAPF	GYYVSDYAMA
			•			
	251	YWGQGTSVTV	SS			

Figure 1B

1	GACATCGTCC	TGACCCAGAG	CCCGGCAAGC	CTGGCTGTTT	CCCTGGGCCA
51	GCGTGCCACT	ATGTCCTGCA	GAGCGGGTGA	GTCTGTTGAC	ATTTTCGGTG
101 .	TCGGTTTTCT	GCACTGGTAC	CAACAGAAAC	CGGGTCAGCC	GCCAAAACTG
151	CTGATCTATC	GTGCTTCTAA	CCTGGAGTCC	GGCATCCCGG	TACGTTTCTC
201	CGGTACTGGC	TCTCGTACTG	ATTTTACCCT	GATTATCGAC	CCGGTGGAAG
251	CAGACGATGT	TGCCACCTAC	TATTGCCAGC	AGACCAACGA	GGATCCGTAC
301	ACCTTCGGTG	GCGGTACTAA	ACTGGAGATC	AAAGGCGGTG	GTGGTTCTGG
351	TGGTGGTGGT	AGCGGCGGCG	GTGGTAGCGG	TGGCGGTGGC	AGCGGTGGTG
401	GTGGCTCTGG	TGGCGGTGGC	TCTGAAGTGC	AGCTGCAGCA	GTCCGGTGCG
451	GAGCTCGTTG	AACCGGGCGC	TTCTGTGAAA	CTGTCTTGCA	CTGCATCTGG
501	TTTCAACATT	AAGGACACCT	ACATGCACTG	GGTGAAACAA	CGCCCGGAAC
551	AGGGTCTGGA	GTGGATCGGT	CGCATCGATC	CGGCTAACGG	TAACAGCAAA
601	TACGTGCCAA	AATTCCAGGG	TAAAGCAACC	ATCACTGCTG	ATACCTCCTC
651	TAACACTGCT	TACCTGCAGC	TGACTTCCCT	GACTAGCGAA	GACACCGCGG
701	TTTATTACTG	CGCTCCGTTC	GGCTACTATG	TCAGCGATTA	CGCAATGGCC
751	TACTGGGGTC	AGGGCACCTC	TGTTACCGTT	TCTAGC	

Figure 1C

263	TPVSEKQL A	EVVANTITP L	MKAQSVPGM A	VAVIYQGKP	
301	HYYTFGKADI	AANKPVTPQT	LFELGSISKT	FTGVLGGDAI	ARGEISLDDA
351	VTRYWPQLTG	KQWQGIRMLD	LATYTAGGLP	LQVPDEVTDN	ASLLRFYQNW
401	QPQWKPGTTR	LYANASIGLF	GALAVKPSGM	PYEQAMTTRV	LKPLKLDHTW
451	INVPKAEEAH	YAWGYRDGKA	VRVSPGMLDA	QAYGVKTNVQ	DMANWVMANM
501	APENVADASL	KQGIALAQSR	YWRIGSMYQG	LGWEMLNWPV	EANTVVETSF
551	GNVALAPLPV	ÄEVNPPAPPV	KASWVHKTGS	TGGFGSYVAF	IPEKQIGIVM
602	LANTSYPNPA	RVEAAYHILE	ALQ		

Figure 1D

1	ACACCGGTGT	CAGAAAAACA	GCTGGCGGAG	GTGGTCGCGA	ATACGATTAC
_	CCCGCTGATG	AAAGCCCAGT	CTGTTCCAGG	CATGGCGGTG	GCCGTTATTT
51	-				·
101	ATCAGGGAAA	ACCGCACTAT	TACACATTTG	GCAAGGCCGA	TATCGCGGCG
.151	AATAAACCCG	TTACGCCTCA	GACCCTGTTC	GAGCTGGGTT	CTATAAGTAA
201	AACCTTCACC	GGCGTTTTAG	GTGGGGATGC	CATTGCTCGC	GGTGAAATTT
251	CGCTGGACGA	TGCGGTGACC	AGATACTGGC	CACAGCTGAC	GGGCAAGCAG
301	TGGCAGGGTA	TTCGTATGCT	GGATCTCGCC	ACCTACACCG	CTGGCGGCCT
351	GCCGCTACAG	GTACCGGATG	AGGTCACGGA	TAACGCCTCC	CTGCTGCGCT
401	TTTATCAAAA	CTGGCAGCCG	CAGTGGAAGC	CTGGCACAAC	GCGTCTTTAC
451	GCCAACGCCA	GCATCGGTCT	TTTTGGTGCG	CTGGCGGTCA	AACCTTCTGG
501	CATGCCCTAT	GAGCAGGCCA	TGACGACGCG	GGTCCTTAAG	CCGCTCAAGC
551	TGGACCATAC	CTGGATTAAC	GTGCCGAAAG	CGGAAGAGGC	GCATTACGCC
601	TGGGGCTATC	GTGACGGTAA	AGCGGTGCGC	GTTTCGCCGG	GTATGCTGGA
651	TGCACAAGCC	TATGGCGTGA	AAACCAACGT	GCAGGATATG	GCGAACTGGG
701	TCATGGCAAA	CATGGCGCCG	GAGAACGTTG	CTGATGCCTC	ACTTAAGCAG
751	GGCATCGCGC	TGGCGCAGTC	GCGCTACTGG	CGTATCGGGT	CAATGTATCA
801	GGGTCTGGGC	TGGGAGATGC	TCAACTGGCC	CGTGGAGGCC	AACACGGTGG
851	TCGAGACGAG	TTTTGGTAAT	GTAGCACTGG	CGCCGTTGCC	CGTGGCAGAA
901	GTGAATCCAC	CGGCTCCCCC	GGTCAAAGCG	TCCTGGGTCC	ATAAAACGGG
951	CTCTACTGGC	GGGTTTGGCA	GCTACGTGGC	CTTTATTCCT	GAAAAGCAGA
1001	TCGGTATTGT	GATGCTCGCG	AATACAAGCT	ATCCGAACCC	GGCACGCGTT
1051	GAGGCGGCAT	ACCATATCCT	CGAGGCGCTA	CAG	

Figure 1E

1	DIVLTQSPAS	LAVSLGQRAT	MSCRAGESVD	IFGVGFLHWY	QQKPGQPPKL
-	•				
51	LIYRASNLES	GIPVRFSGTG	SRTDFTLIID	PVEADDVATY	YCQQTNEDPY
101	TFGGGTKLEI	KGGGGSGGG	SGGGSGGG	SGGGSGGG	SEVQLQQSGA
151	i	LSCTASGFNI			
201	YVPKFQGKAT	ITADTSSNTA	YLQLTSLTSE	DTAVYYCAPF	GYYVSDYAMA
251	YWGQGTSVTV	<u>SS</u> TPVSEKQL	AEVVANTITP	LMKAQSVPGM	AVAVIYQGKP
301	HŸYTFGKADI	AANKPVTPQT	LFELGSISKT	FTGVLGGDAI	ARGEISLDDA
351	VTRYWPQLTG	KQWQGIRMLD	LATYTAGGLP	LQVPDEVTDN	ASLLRFYQNW
401	QPQWKPGTTR	LYANASIGLF	GALAVKPSGM	PYEQAMTTRV	LKPLKLDHTW
451	INVPKAEEAH	YAWGYRDGKA	VRVSPGMLDA	QAYGVKTNVQ	DMANWVMANM
501	APENVADASL	KQGIALAQSR	YWRIGSMYQG	LGWEMLNWPV	EANTVVETSF
551	GNVALAPLPV	AEVNPPAPPV	KASWVHKTGS	TGGFGSYVAF	IPEKQIGIVM
601	LANTSYPNPA	RVEAAYHILE	ALQ ·		

Figure 1F

	·			
		TGACCCAGAG	CCCGGCAAGC	CTGGCTGTTT
CCCTGG				·
- - ·		ATGTCCTGCA	GAGCGGGTGA	GTCTGTTGAC
ATTTTC		•	•	•
101 TCG	GTTTTCT	GCACTGGTAC	CAACAGAAAC	CGGGTCAGCC
GCCAAA		•		•
151 CTG	ATCTATC	GTGCTTCTAA	CCTGGAGTCC	GGCATCCCGG
TACGTT'				•
201 CGG	TACTGGC	TCTCGTACTG	ATTTTACCCT	GATTATCGAC
CCGGTG		A shipmanian A s a b	other more and most	
251 CAG	ACGATGT	TGCCACCTAC	TATTGCCAGC	AGACCAACGA
GGATCC			•	•
301 ACC	TTCGGTG	GCGGTACTAA	ACTGGAGATC	AAAGGCGGTG
GTGGTT		•		•
351 TGG	TGGTGGT	AGCGGCGGCG	GTGGTAGCGG	TGGCGGTGGC
AGCGGT	GGTG			
401 GTG	GCTCTGG	TGGCGGTGGC	TCTGAAGTGC	AGCTGCAGCA
GTCCGG'		,		
451 GAG	CTCGTTG	AACCGGGCGC	TTCTGTGAAA	CTGTCTTGCA
CTGCAT		•		
501 TTT	CAACATT	AAGGACACCT	ACATGCACTG	GGTGAAACAA
CGCCCG			-	
551 AGG	GTCTGGA	GTGGATCGGT	CGCATCGATC	CGGCTAACGG
TAACAG		•		•
601 TAC	GTGCCAA	AATTCCAGGG	TAAAGCAACC	ATCACTGCTG
ATACCTO			•	•
651 TAA	CACTGCT	TACCTGCAGC	TGACTTCCCT	GACTAGCGAA
GACACC				
, •		CGCTCCGTTC	GGCTACTATG	TCAGCGATTA
CGCAATO				
	•	AGGGCACCTC	TGTTACCGTT	TCTAGCACAC
CGGTGTC				
		GCGGAGGTGG	TCGCGAATAC	GATTACCCCG
CTGATGA	AAG			
		TCCAGGCATG	GCGGTGGCCG	TTATTTATCA
GGGAAAA				
		CATTTGGCAA	GGCCGATATC	GCGGCGAATA
AACCCGI	TAC			
		CTGTTCGAGC	TGGGTTCTAT	AAGTAAAACC
TTCACCG	GCG			
		GGATGCCATT	GCTCGCGGTG	AAATTTCGCT
GGACGAT	'GCG			
		ACTGGCCACA	GCTGACGGGC	AAGCAGTGGC
AGGGTAT	TCG '		*	

1101	TATGCTGGAT	CTCGCCACCT	ACACCGCTGG	CGGCCTGCCG
CTA	ACAGGTAC		•	
1151	CGGATGAGGT	CACGGATAAC	GCCTCCCTGC	TGCGCTTTTA
	AAACTGG			
1201	CAGCCGCAGT	GGAAGCCTGG	CACAACGCGT	CTTTACGCCA
	GCCAGCAT			
1251	CGGTCTTTTT	GGTGCGCTGG	CGGTCAAACC	TTCTGGCATG
	CTATGAGC		•	
	AGGCCATGAC	GACGCGGGTC	CTTAAGCCGC	TCAAGCTGGA
	ATACCTGG			
	ATTAACGTGC	CGAAAGCGGA	AGAGGCGCAT	TACGCCTGGG
	PATCGTGA			~~~~~~~~~~~
	CGGTAAAGCG	GTGCGCGTTT	CGCCGGGTAT	GCTGGATGCA
CAZ	AGCCTATG	·		7.0000000000
	GCGTGAAAAC	CAACGTGCAG	GATATGGCGA	ACTGGGTCAT
	CAAACATG	7 CCMMCCMC7	m C C C M C M C M M	א א כיכא כיכיכיא
	GCGCCGGAGA	ACGTTGCTGA	TGCCTCACTT	AAGCAGGCA
	GCAGTCGCGC	ma cmccccma	መሮርርርምርን ንጥ	CTATCACCCT
		TACTGGCGTA	ICGGGICAAI	GINICAGGGI
CTO	GGGCTGGG AGATGCTCAA	CTCCCCCTTC	CACCCCAACA	СССТССТССА
	CGAGTTTT	CIGGCCCGIG	GAGGCCAACA	0001001001
1 C E 1	GGTAATGTAG	CACTEGCECC	GTTGCCCGTG.	GCAGAAGTGA
	CCACCGGC	Cheredees	0110000010	•
1701	TCCCCCGGTC	AAAGCGTCCT	GGGTCCATAA	AACGGGCTCT
-	rggcgggT			•
1751	TTGGCAGCTA	CGTGGCCTTT	ATTCCTGAAA	AGCAGATCGG
TA!	TTGTGATG			
1801	CTCGCGAATA	CAAGCTATCC	GAACCCGGCA	CGCGTTGAGG
	GCATACCA			
1851	TATCCTCGAG	GCGCTACAG		

Figure 2A

	118417 21-								
DIVLTO	DIVLTQSPAS LSVSLGQRAT MSCRAGESVD IFGVGFLHWY QQKPGQPPKL								
51	LIYRASNLES	GIPVRFSGTG	SGTDFTLIID	PVEADDVATY	YCQQTNEDPY				
101	TFGGGTKLEI	KGGGGSGGG	SGGGGSGGG	SGGGSGGG	SEVQLQQSGA				
151	ELVEPGASVK	LSCTASGFNI	KDTYMHWVKQ	RPEQGLEWIG	RIDPANGNSK				
201	YVPKFQGKAT	ITADTSSNTA	YLQLTSLTSE	DTAVYYCAPF	GYYVSDYAMA				
251	YWGQGTSVTV	ss		•					

Figure 2B

1	GACATCGTCC	TGACCCAGAG	CCCGGCAAGC	CTGTCTGTTT	CCCTGGGCCA
51	GCGTGCCACT	ATGTCCTGCA	GAGCGGGTGA	GTCTGTTGAC	ATTTTCGGTG
101	TCGGTTTTCT	GCACTGGTAC	CAACAGAAAC	CGGGTCAGCC	GCCAAAACTG
151	CTGATCTATC	GTGCTTCTAA	CCTGGAGTCC	GGCATCCCGG	TACGTTTCTC
201	CGGTACTGGC		ATTTTACCCT	GATTATCGAC	CCGGTGGAAG
251	CAGACGATGT	TGCCACCTAC	TATTGCCAGC	AGACCAACGA	GGATCCGTAC
301	ACCTTCGGTG	GCGGTACTAA	ACTGGAGATC	AAAGGCGGTG	GTGGTTCTGG
351	TGGTGGTGGT	AGCGGTGGCG	GTGGTAGCGG	TGGCGGTGGC	AGCGGTGGTG
401	GTGGCTCTGG	TGGCGGTGGC		AGCTGCAGCA	
451	GAGCTCGTTG	AACCGGGCGC		CTGTCTTGCA	CTGCATCTGG
501	TTTCAACATT	AAGGACACCT		GGTGAAACAA	
551	AGGGTCTGGA	GTGGATCGGT		CGGCTAACGG	
		AATTCCAGGG	TAAAGCAACC	ATCACTGCTG	ATACCTCCTC
601	TAACACTGCT	TACCTGCAGC	TGACTTCCCT	GACTAGCGAA	GACACCGCGG
651	TTTATTACTG		GGCTACTATG	TCAGCGATTA	CGCAATGGCC
701 751		AGGGCACCTC		TCTAGC	
/ n	T ALC T Let et et et et la la	TOUGO TO TO			

Figure 3

TPVSEKQL AEVVANTITP LMAAQSVPGM AVAVIYQGKP

301 HYYTFGKADI AANKPVTPQT LFELGSISKT FTGVLGGDAI ARGEISLDDA

351 VTRYWPQLTG KQWQGIRMLD LATYTAGGLP LQVPDEVTDN ASLLRFYQNW

401 QPQWKPGTTR LYANASIGLF GALAVKPSGM PYEQAMTTRV LKPLKLDHTW

451 INVPKAEEAH YAWGYRDGKA VRVSPGMLDA QAYGVKTNVQ DMANWVMANM

501 APENVADASL KQGIALAQSR YWRIGSMYQG LGWEMLNWPV EANTVVETSF

551 GNVALAPLPV AEVNPPAPPV KASWVHKTGS TGGFGAYVAF IPEKQIGIVM

601 LANTSYPNPA RVEAAYHILE ALQ

Figure 4A

1	DIVLTQSPAS	LSVSLGQRAT	MSCRAGESVD	TEGAGETHMA	QQKPGQPPKL
51	LIYRASNLES				
101_	TFGGGTKLEI	K <i>GGGGSGGG</i>	SGGGSGGGG	SGGGSGGGG	SEVQLQQSGA
151	ELVEPGASVK	LSCTASGFNI	KDTYMHWVKQ	RPEQGLEWIG	RIDPANGNSK
201_	YVPKFQGKAT	ITADTSSNTA	YLQLTSLTSE	DTAVYYCAPF	GYYVSDYAMA
251_	YWGQGTSVTV	SSTPVSEKQL	AEVVANTITP	LMKAQSVPGM	AVAVIYQGKP
301	HYYTFGKADI	AANKPVTPQT	LFELGSISKT	FTGVLGGDAI	ARGEISLDDA
351	VTRYWPQLTG	KQWQGIRMLD	LATYTAGGLP	LQVPDEVTDN	ASLLRFYQNW
401	QPQWKPGTTR	LYANASIGLE	GALAVKPSGM	PYEQAMTTRV	LKPLKLDHTW
451	INVPKAEEAH	YAWGYRDGKA	VRVSPGMLDA	QAYGVKTNVQ	MAMWVMAMM
501	APENVADASL	KQGIALAQSR	YWRIGSMYQG	LGWEMLNWPV	EANTVVETSF
551	GNVALAPLPV	AEVNPPAPPV	KASWVHKTGS	TGGFGSYVAF	' IPEKQIGIVM
601	LANTSYPNPA	RVEAAYHILE	ALQ		·

Figure 4B

1.	GACATCGTC	C TGACCCAGAG	CCCGGCAAGC	CTGTCTGTTT	CCCTGGGCCA
51	GCGTGCCAC	T ATGTCCTGCA	GAGCGGGTGA	GTCTGTTGAC	ATTTTCGGTG
101	TCGGTTTTC	T GCACTGGTAC	CAACAGAAAC	CGGGTCAGCC	GCCAAAACTG
151	CTGATCTAT	C GTGCTTCTAA	CCTGGAGTCC	GGCATCCCGG	TACGTTTCTC
201	CGGTACTGG	C TCTGGTACTG	ATTTTACCCT	GATTATCGAC	CCGGTGGAAG
251	CAGACGATG	T TGCCACCTAC	TATTGCCAGC	AGACCAACGA	GGATCCGTAC
301	ACCTTCGGT	G GCGGTACTAA	ACTGGAGATC	AAAGGCGGTG	GTGGTTCTGG
351	TGGTGGTGG	T AGCGGTGGCG	GTGGTAGCGG	TGGCGGTGGC	AGCGGTGGTG
401	GTGGCTCTG	G TGGCGGTGGC	TCTGAAGTGC	AGCTGCAGCA	GTCCGGTGCG
451	- GAGCTCGTT	G AACCGGGCGC	TTCTGTGAAA	CTGTCTTGCA	CTGCATCTGG
501	TTTCAACAT	r aaggacacct	ACATGCACTG	GGTGAAACAA	CGCCCGGAAC
551	AGGGTCTGG	A GTGGATCGGT	CGCATCGATC	CGGCTAACGG	TAACAGCAAA
601	TACGTGCCA	A AATTCCAGGG	TAAAGCAACC	ATCACTGCTG	ATACCTCCTC
651	TAACACTGC:	TACCTGCAGC	TGACTTCCCT	GACTAGCGAA	GACACCGCGG
701	TTTATTACTO	G CGCTCCGTTC	GGCTACTATG	TCAGCGATTA	CGCAATGGCC
751	TACTGGGGT	CAGGGCACCTC	TGTTACCGTT	TCTAGCACAC	CGGTGTCAGA
801	AAAACAGCT	G GCGGAGGTGG	TCGCGAATAC	GATTACCCCG	CTGATGAAAG
851	CCCAGTCTG:	TCCAGGCATG	GCGGTGGCCG	TTATTTATCA	GGGAAAACCG
901	CACTATTACA	A CATTTGGCAA	GGCCGATATC	GCGGCGAATA	AACCCGTTAC
951	GCCTCAGACO	CTGTTCGAGC	TGGGTTCTAT	AAGTAAAACC	TTCACCGGCG
1001	TTTTAGGTG	GGATGCCATT	GCTCGCGGTG	AAATTTCGCT	GGACGATGCG
1051	GTGACCAGAT	ACTGGCCACA	GCTGACGGGC	AAGCAGTGGC	AGGGTATTCG
1101	TATGCTGGAT	CTCGCCACCT	ACACCGCTGG	CGGCCTGCCG	CTACAGGTAC
1151	CGGATGAGGT	CACGGATAAC	GCCTCCCTGC	TGCGCTTTTA	TCAAAACTGG
1201	CAGCCGCAGI	GGAAGCCTGG	CACAACGCGT	CTTTACGCCA	ACGCCAGCAT
1251	CGGTCTTTT	GGTGCGCTGG	CGGTCAAACC		CCCTATGAGC
1301	AGGCCATGAC	GACGCGGGTC	CTTAAGCCGC	TCAAGCTGGA	CCATACCTGG
1351	ATTAACGTGC	CGAAAGCGGA	AGAGGCGCAT	TACGCCTGGG	GCTATCGTGA
1401	CGGTAAAGCG	GTGCGCGTTT	CGCCGGGTAT	GCTGGATGCA	CAAGCCTATG
1451	GCGTGAAAAC		GATATGGCGA	ACTGGGTCAT	GGCAAACATG
1501	GCGCCGGAGA		TGCCTCACTT	AAGCAGGGCA	TCGCGCTGGC
1551·	GCAGTCGCGC		TCGGGTCAAT	GTATCAGGGT	CTGGGCTGGG
1601	AGATGCTCAA		GAGGCCAACA	CGGTGGTCGA	
1651	GGTAATGTAG		GTTGCCCGTG	GCAGAAGTGA	ATCCACCGGC
1701	TCCCCCGGTC		GGGTCCATAA		ACTGGCGGGT
1751	TTGGCAGCTA		ATTCCTGAAA		TATTGTGATG
1801	CTCGCGAATA		GAACCCGGCA	CGCGTTGAGG	CGGCATACCA
1851	TATCCTCGAG	GCGCTACAG			·
•					

Figure 4C

1	DIVLTQSPAS	L S VSLGQRAT	MSCRAGESVD_	IFGVGFLHWY	QQKPGQPPKL
-			*	•	
51	LIYRASNLES	GIPVRFSGTG	S G TDFTLIID	PVEADDVATY	YCQQTNEDPY
				:	
101	TFGGGTKLEI	KGGGGSGGG	SGGGGSGGG	SGGGSGGG	SEVQLQQSGA
151	ELVEPGASVK	LSCTASGFNI	KDTYMHWVKQ	RPEQGLEWIG	RIDPANGNSK
201	YVPKFQGKAT	ITADTSSNTA	YLQLTSLTSE	DTAVYYCAPF	GYYVSDYAMA
251	YWGQGTSVTV	<u>SS</u> TPVSEKQL	AEVVANTITP	LM A AQSVPGM	AVAVIYQGKP
301	HYYTFGKADI	AANKPVTPQT	LFELGSISKT	FTGVLGGDAI	ARGEISLDDA
351	VTRYWPQLTG	KQWQGIRMLD	LATYTAGGLP	LQVPDEVTDN	ASLLRFYQNW
401	QPQWKPGTTR	LYANASIGLF	GALAVKPSGM	PYEQAMTTRV	LKPLKLDHTW
451	INVPKAEEAH	YAWGYRDGKA	VRVSPGMLDA	QAYGVKTNVQ	DMANWVMANM
501	APENVADASL	KQGIALAQSR	YWRIGSMYQG	LGWEMLNWPV	EANTVVETSF
551	GNVALAPLPV	AEVNPPAPPV	KASWVHKTGS	TGGFG A YVAF	IPEKQIGIVM
601	LANTSYPNPA	RVEAAYHILE	ALQ		

Figure 4D

1	GACATCGTCC	TGACCCAGAG	CCCGGCAAGC	CTGTCTGTTT	CCCTGGGCCA
51	GCGTGCCACT	ATGTCCTGCA	GAGCGGGTGA	GTCTGTTGAC	ATTTTCGGTG
101	TCGGTTTTCT	GCACTGGTAC	CAACAGAAAC	CGGGTCAGCC	GCCAAAACTG
151	CTGATCTATC	GTGCTTCTAA	CCTGGAGTCC	GGCATCCCGG	TACGTTTCTC
.201	CGGTACTGGC	TCTGGTACTG	ATTTTACCCT	GATTATCGAC	CCGGTGGAAG
251	CAGACGATGT	TGCCACCTAC	TATTGCCAGC	AGACCAACGA	GGATCCGTAC
301	ACCTTCGGTG	GCGGTACTAA	ACTGGAGATC	AAAGGCGGTG	GTGGTTCTGG
351	TGGTGGTGGT	AGCGGTGGCG	GTGGTAGCGG	TGGCGGTGGC	AGCGGTGGTG
401	GTGGCTCTGG	TGGCGGTGGC	TCTGAAGTGC	AGCTGCAGCA	GTCCGGTGCG
451	GAGCTCGTTG	AACCGGGCGC	TTCTGTGAAA	CTGTCTTGCA	CTGCATCTGG
501	TTTCAACATT	AAGGACACCT	ACATGCACTG	GGTGAAACAA	CGCCCGGAAC
551	AGGGTCTGGA	GTGGATCGGT	CGCATCGATC	CGGCTAACGG	TAACAGCAAA
601	TACGTGCCAA	AATTCCAGGG	TAAAGCAACC	ATCACTGCTG	ATACCTCCTC
651	TAACACTGCT	TACCTGCAGC	TGACTTCCCT	GACTAGCGAA	GACACCGCGG
701	TTTATTACTG	CGCTCCGTTC	GGCTACTATG	TCAGCGATTA	CGCAATGGCC
751	TACTGGGGTC	AGGGCACCTC	TGTTACCGTT	TCTAGCACAC	CGGTGTCAGA
801	AAAACAGCTG	GCGGAGGTGG	TCGCGAATAC	GATTACCCCG	CTGATGGCGG
851	CCCAGTCTGT	TCCAGGCATG	GCGGTGGCCG	TTATTTATCA	GGGAAAACCG
901	CACTATTACA		GGCCGATATC	GCGGCGAATA	AACCCGTTAC
951	GCCTCAGACC	CTGTTCGAGC	TGGGTTCTAT	AAGTAAAACC	TTCACCGGCG
1001	TTTTAGGTGG	GGATGCCATT	GCTCGCGGTG	AAATTTCGCT	GGACGATGCG
1051	GTGACCAGAT	ACTGGCCACA	GCTGACGGGC	AAGCAGTGGC	AGGGTATTCG
1101	TATGCTGGAT	CTCGCCACCT		CGGCCTGCCG	CTACAGGTAC
1151	CGGATGAGGT	CACGGATAAC	GCCTCCCTGC	TGCGCTTTTA	TCAAAACTGG
1201	CAGCCGCAGT	GGAAGCCTGG	CACAACGCGT	CTTTACGCCA	ACGCCAGCAT
1251	CGGTCTTTTT	GGTGCGCTGG	CGGTCAAACC	TTCTGGCATG	CCCTATGAGC
1301	AGGCCATGAC	GACGCGGGTC	CTTAAGCCGC	TCAAGCTGGA	CCATACCTGG
1351	ATTAACGTGC	CGAAAGCGGA	AGAGGCGCAT	TACGCCTGGG	GCTATCGTGA
1401	CGGTAAAGCG	GTGCGCGTTT	CGCCGGGTAT	GCTGGATGCA	CAAGCCTATG
1451	GCGTGAAAAC	CAACGTGCAG	GATATGGCGA	ACTGGGTCAT	GGCAAACATG
1501	GCGCCGGAGA	ACGTTGCTGA	TGCCTCACTT	AAGCAGGGCA	TCGCGCTGGC
1551	GCAGTCGCGC	TACTGGCGTA	TCGGGTCAAT	GTATCAGGGT	CTGGGCTGGG
1601	AGATGCTCAA	CTGGCCCGTG	GAGGCCAACA	CGGTGGTCGA	GACGAGTTTT
1651	GGTAATGTAG	CACTGGCGCC	GTTGCCCGTG	GCAGAAGTGA	ATCCACCGGC
1701	TCCCCCGGTC	AAAGCGTCCT	GGGTCCATAA	AACGGGCTCT	ACTGGCGGGT
1751	TTGGCGCGTA	CGTGGCCTTT	ATTCCTGAAA	AGCAGATCGG	TATTGTGATG
1801	CTCGCGAATA	CAAGCTATCC	GAACCCGGCA	CGCGTTGAGG	CGGCATACCA
1851	TATCCTCGAG	GCGCTACAG	•		

Figure 4E

1 AGGAATTATO CTGGTCTGCT	C ATATGAAATA	CCTGCTGCCG	ACCGCTGCTG
51 GCTCCTCGCT ACCCAGAGCC	r GCCCAGCCGG	CCATGGCCGA	CATCGTCCTG
101 CGGCAAGCC GTCCTGCAGA	r grctgtttcc	CTGGGCCAGC	GTGCCACTAT
151 GCGGGTGAG ACTGGTACCA	r ctgttgacat	TTTCGGTGTC	GGTTTTCTGC
201 ACAGAAACCO GCTTCTAACC	G GGTCAGCCGC	CAAAACTGCT	GATCTATCGT
251 TGGAGTCCGG TGGTACTGAT	G CATCCCGGTA	CGTTTCTCCG	GTACTGGCTC
301 TTTACCCTGA CCACCTACTA	A TTATCGACCC	GGTGGAAGCA	GACGATGTTG
351 TTGCCAGCAG GGTACTAAAC	G ACCAACGAGG	ATCCGTACAC	CTTCGGTGGC
401 TGGAGATCA	A AGGCGGTGGT	GGTTCTGGTG	GTGGTGGTAG
451 GGTAGCGGTC GCGGTGGCTC	G GCGGTGGCAG	CGGTGGTGGT	GGCTCTGGTG
501 TGAAGTGCAG CCGGGCGCTT	G CTGCAGCAGT	CCGGTGCGGA	GCTCGTTGAA
551 CTGTGAAAC' GGACACCTAC	r GTCTTGCACT	GCATCTGGTT	TCAACATTAA
601 ATGCACTGGC GGATCGGTCG	G TGAAACAACG	CCCGGAACAG	GGTCTGGAGT
651 CATCGATCC	G GCTAACGGTA	ACAGCAAATA	CGTGCCAAAA
701 AAGCAACCAT CCTGCAGCTG	CACTGCTGAT	ACCTCCTCTA	ACACTGCTTA
751 ACTTCCCTGA CTCCGTTCGG	A CTAGCGAAGA	CACCGCGGTT	TATTACTGCG
801 CTACTATGTO	AGCGATTACG	CAATGGCCTA	CTGGGGTCAG
851 TTACCGTTT(GGAGGTGGTC	· v		
901 GCGAATACGA CAGGCATGGC	TTACCCCGCT	GATGGCGGCC	CAGTCTGTTC
951 GGTGGCCGTT	T ATTTATCAGG	GAAAACCGCA	CTATTACACA
1001 CCGATATCGC GTTCGAGCTG	C GGCGAATAAA	CCCGTTACGC	CTCAGACCCT

1051	GGTTCTATAA TGCCATTGC	GTAAAACCTT	CACCGGCGTT	TTAGGTGGGG
		3 MMMCCCMCC	ACCAMCCCCM	GACCAGATAC
T	TCGCGGTGAA GGCCACAGC		•	
1151	TGACGGGCAA	GCAGTGGCAG	GGTATTCGTA	TGCTGGATCT
C	GCCACCTAC	ı		•
1201	ACCGCTGGCG	GCCTGCCGCT	ACAGGTACCG	GATGAGGTCA
C	GGATAACGC			• .
1251	CTCCCTGCTG	CGCTTTTATC	AAAACTGGCA	GCCGCAGTGG
	AGCCTGGCA			
	CAACGCGTCT	TTACGCCAAC	GCCAGCATCG	GTCTTTTTGG
	GCGCTGGCG		•	
	GTCAAACCTT	CTGGCATGCC	CTATGAGCAG	GCCATGACGA
	GCGGGTCCT			
	TAAGCCGCTC	AAGCTGGACC	ATACCTGGAT	TAACGTGCCG
	AAGCGGAAG	111.001.001.00		:
1/51	AGGCGCATTA	СССТССССССССССССССССССССССССССССССССССС	TATCGTGACG	GTAAAGCGGT
	CGCGTTTCG			
		тссатссаса	AGCCTATGGC	GTGAAAACCA
1501	CGTGCAGGA	1001110011011	1100011111000	01011110011
		TGGGTCATGG	CAAACATGGC	GCCGGAGAAC
1551	TTGCTGATG		CIMMICHIEGO	000001191210
7.001	CCTCACTTAA	CCACCCCATC	CCCCTCCCCC	AGTCGCGCTA
		GCAGGGCAIC	000010000	1101 00000111
	TGGCGTATC	ATCAGGGTCT	GGGCTGGGAG	ΔͲ ϹϹͲϹ Δ Δ ϹͲ
	GGGTCAATGT	MICAGGICI	GGGCIGGGAG	HICTOMICI
G	GCCCGTGGA GGCCAACACG	CHCCHCCACA	ССАСФФФФСС	ͲϪϪͲϹͲϪϹϹϪ
		GIGGICGMGA	CGAGIIIIGG	
C	TGCCCGTGGC	7 C 7 7 C C C 7 7 M	CCACCCCCTC	CCCCGGTCAA
		AGAAGIGAAI	CCACCGGCIC	CCCCGGICAM
A	GCGTCCTGG GTCCATAAAA	CCCCCTCTAC		GCCCCCTACC.
		CGGGCTCTAC	166666111	. GGCGCGIACG
-	GGCCTTTAT	CT CT MOCCOT	mmcmc»mccm	CGCGAATACA
1851		CAGATCGGTA	TIGIGATGCT	CGCGAAIACA
A	GCTATCCGA	COMMON COOC	CCAMACCAMA	THE CTICE A CCC
	ACCCGGCACG	CGTTGAGGCG	GCATACCATA	1CC1CGAGGC
G	CTACAGTAG		7 CCERTCCCCC	CCCACTICCAC
	GAATTCGAGC	TCCGTCGACA	AGCTTGCGGC	CGCACTCGAG
A	TCAAACGGG		~~~~~~~~	
	CTAGCCAGCC	AGAACTCGCC	CCGGAAGACC	CCGAGGATGT
С	GAGCACCAC			
	CACCACCACC	ACTGAGATCC	GGCTGCTAAC	AAAGCCCGAA
A	GGAAGCTGA			•
	GTTGGCTGCT	GCCACCGCTG	AGCAATAACT	AGCATAACCC
C	TTGGGGCCT		•	
2151	CTAAACGGGT	CTTGAGGGGT	TTTTTGCTGA	AAGGAGGAAC
	ATATCCGGA			

	TTGGCGAATG CGGGTGTG	GGACGCGCCC	TGTAGCGGCG	CATTAAGCGC
			000E2020E	
	GTGGTTACGC GCGCCCGC	GCAGCGTGAC	CGCTACACTT	GCCAGCGCCC
	TCCTTTCGCT	ՠՠ ՀՠՠՀ ՀՀ Հապ	CCTTTCTCGC	$C\Delta CGTTCGCC$
GG	CTTTCCCC			
2351	GTCAAGCTCT	AAATCGGGGG	CTCCCTTTAG	GGTTCCGATT
	GTGCTTTA			
0401	CGGCACCTCG	7 CCCC7 7 7 7 7 7	א כידייים אידייא כ	CCTCNTCCTT
		ACCCCAAAAA	ACTIGNTING	GGIGAIGGII
	CGTAGTGG			
2451	GCCATCGCCC	TGATAGACGG	TTTTTCGCCC	TTTGACGTTG
GA	GTCCACGT			•
	TCTTTAATAG	TEGACTETTE	TTCCAAACTG	GAACAACACT
	ACCCTATC			
			3 M 3 A C C 3 M M	mmcocca mmm
	TCGGTCTATT	CTTTTGATTT	ATAAGGGATT	TTGCCGATTT
	GCCTATTG			•
2601	GTTAAAAAAT	GAGCTGATTT	AACAAAAATT	TAACGCGAAT
•	raacaaaa			
	TATTAACGCT	ጥልሮል ልጥጥጥሮሮ	TGATGCGGTA	Պարար ԸՊԸՊա
		1110111111100	101110000111	
	GCATCTGT			
	GCGGTATTTC	ACACCGCATA	TGGTGCACTC	TCAGTACAAT
-	GCTCTGAT			
2751	GCCGCATAGT	TAAGCCAGCC	CCGACACCCG	CCAACACCCG
СТО	GACGCGCC			
	CTGACGGGCT	тстстсстсс	CGGCATCCGC	TTACAGACAA
	rgtgaccg	1010100100		
		cmcci mcmcm		CACCCCCACA
	TCTCCGGGAG	CTGCATGTGT	CAGAGGIIII	CACCGICATC
	CGAAACGC	•		
2901	GCGAGACGAA	AGGGCCTCGT	GATACGCCTA	TTTTTATAGG
ТТА	AATGTCAT	:		
	GATAATAATG	GTTTCTTAGA	CGTCAGGTGG	CACTTTTCGG
	AAATGTGC	0111011011	•••	
				MACAMMCAAA
	GCGGAACCCC	TATTIGTTTA	TTTTTCTAAA	IACAIICAAA
	rgtatccg			
3051	CTCATGAGAC	AATAACCCTG	TGGCAGCATC	ACCCGACGCA
CTT	TGCGCCG	•	•	
3101	AATAAATACC	TGTGACGGAA	GATCACTTCG	CAGAATAAAT
	ATCCTGGT			,
AAA	41CC1GG1	7 M7 CCCCC7 7	COCOMCCCCC	7 7 CMMMMCCC
	GTCCCTGTTG	ATACCGGGAA	GCCCTGGGCC	AACTITIGGC
	AATGAGA	•		
3201	CGTTGATCGG	CACGTAAGAG	GTTCCAACTT	TCACCATAAT
	ATAAGAT	•		
	CACTACCGGG	CCADAdanaaaa	САСТТАТССА	GATTTTCAGG
	TAAGGAA		an amaan ===============================	7 007 000mm
	GCTAAAATGG	AGAAAAAAAT	CACTGGATAT	ACCACCGTTG
ATA	ATATCCCA			

3351 ATGGCATCGT AAAGAACATT TTGAGGCATT TC GCTCAATGTA 3401 CCTATAACCA GACCGTTCAG CTGGATATTA CG	GGCCTTTTT
3401 CCTATAACCA GACCGTTCAG CTGGATATTA CG	
AAAGACCGTA	•
	ጥጥልጥጥርልርል
9.92	1 1111 1 011011
TTCTTGCCCG 3501 CCTGATGAAT GCTCATCCGG AATTCCGTAT GG	ירכא איזיכא א א
3001 001 111	GCAALGAAA
GACGGTGAGC	
3551 TGGTGATATG GGATAGTGTT CACCCTTGTT AC	CACCGITII
CCATGAGCAA	
3601 ACTGAAACGT TTTCATCGCT CTGGAGTGAA TA	ACCACGACG
ATTTCCGGCA	
3651 GTTTCTACAC ATATATTCGC AAGATGTGGC GT	TGTTACGGT
GAAAACCTGG	•
3701 CCTATTTCCC TAAAGGGTTT ATTGAGAATA TO	GTTTTTCGT
CTCAGCCAAT	•
3751 CCCTGGGTGA GTTTCACCAG TTTTGATTTA AF	ACGTGGCCA
ATATGGACAA	
3801 CTTCTTCGCC CCCGTTTTCA CGATGGGCAA AT	TATTATACG
CAAGGCGACA	
3851 AGGTGCTGAT GCCGCTGGCG ATTCAGGTTC AT	TCATGCCGT
CTGTGATGGC	
3901 TTCCATGTCG GCAGAATGCT TAATGAATTA CA	AACAGTACT
GCGATGAGTG	
3951 GCAGGGCGGG GCGTAAAGAC AGATCGCTGA GA	ATAGGTGCC
TCACTGATTA	
4001 AGCATTGGTA ACTGTCAGAC CAAGTTTACT CA	ATATATACT
TTAGATTGAT	•
4051 TTAAAACTTC ATTTTTAATT TAAAAGGATC TA	'AGGTGAAGA
TCCTTTTGA	
4101 TAATCTCATG ACCAAAATCC CTTAACGTGA GT	TTTTCGTTC
CACTGAGCGT	
4151 CAGACCCCGT AGAAAAGATC AAAGGATCTT CT	TTGAGATCC
TTTTTTCTG	
4201 CGCGTAATCT GCTGCTTGCA AACAAAAAA CC	CACCGCTAC
CAGCGGTGGT	•
4251 TTGTTTGCCG GATCAAGAGC TACCAACTCT TT	TTTCCGAAG
GTAACTGGCT	:
4301 TCAGCAGAGC GCAGATACCA AATACTGTTC TT	TCTAGTGTA
GCCGTAGTTA	•
4351 GGCCACCACT TCAAGAACTC TGTAGCACCG CC	CTACATACC
TCGCTCTGCT	•
4401 AATCCTGTTA CCAGTGGCTG CTGCCAGTGG CG	GATAAGTCG
TGTCTTACCG	
4451 GGTTGGACTC AAGACGATAG TTACCGGATA AC	GGCGCAGCG
GTCGGGCTGA	
GICGGGCIGV	• •

4501	ACGGGGGGTT	CGTGCACACA	GCCCAGCTTG	GAGCGAACGA
CCI	CACCGA			
4551	ACTGAGATAC	CTACAGCGTG	AGCTATGAGA	AAGCGCCACG
CTI	CCCGAAG		•	
4601	GGAGAAAGGC	GGACAGGTAT	CCGGTAAGCG	GCAGGGTCGG
AAC	CAGGAGAG			
4651	CGCACGAGGG	AGCTTCCAGG	GGGAAACGCC	TGGTATCTTT
AT?	AGTCCTGT		•	
4701	CGGGTTTCGC	CACCTCTGAC	TTGAGCGTCG	ATTTTTGTGA
TG	CTCGTCAG			
4751	GGGGGCGGÀG	CCTATGGAAA	AACGCCAGCA	ACGCGGCCTT
	racggttc			
	CTGGCCTTTT	GCTGGCCTTT	TGCTCACATG	TTCTTTCCTG
CG!	TTATCCCC	•		·
	TGATTCTGTG	GATAACCGTA	TTACCGCCTT	TGAGTGAGCT
GA'	TACCGCTC			· .
	GCCGCAGCCG	AACGACCGAG	CGCAGCGAGT	CAGTGAGCGA
GG	AAGCGGAA			
	GAGCGCCCAA	TACGCAAACC	GCCTCTCCCC	GCGCGTTGGC
CG	ATTCATTA			
	ATGCAGCTGG	CACGACAGGT	TTCCCGACTG	GAAAGCGGGC
AG'	TGAGCGCA			
5051		TGTGAGTTAG	CTCACTCATT	AGGCACCCCA
GG	CTTTACAC			*
	TTTATGCTTC	CGGCTCGTAT	GTTGTGTGGA	ATTGTGAGCG
GA'	TAACAATT			
	TCACACAGGA	AACAGCTATG	ACCATGATTA	CGCCAAGCTA
TT'	TAGGTGAC		mama a a mma a	66
5201	ACTATAGAAT	ACTCAAGCTT	TCTAGATTAA	99

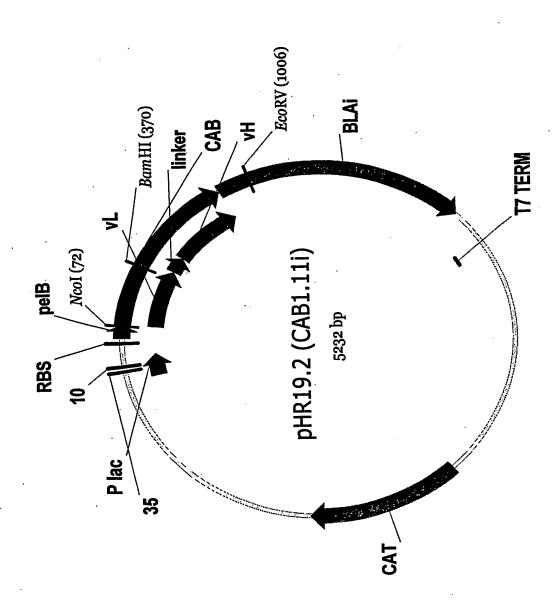
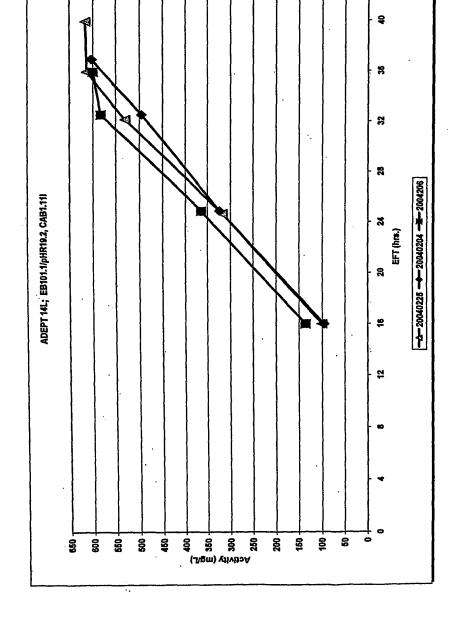


Figure 5

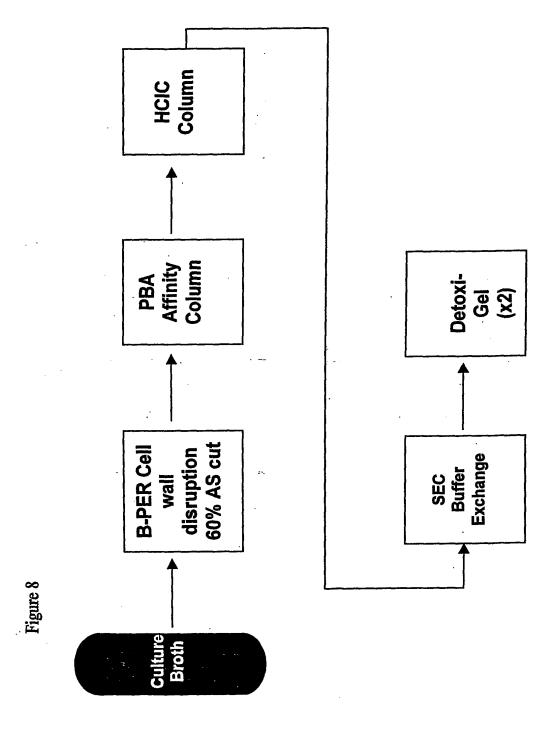
barent CAB1.10 HB14.14 HR14.13 Clone number HR14.10 HR14.9 4R14.8 က sbecitic binding (%)

Figure 6

\$

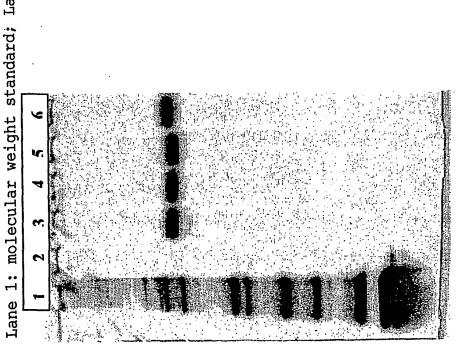


Figure

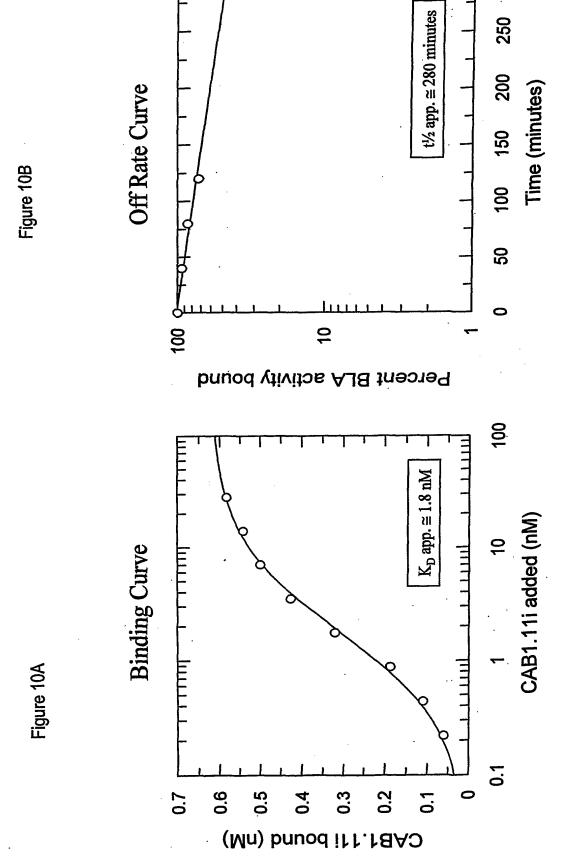


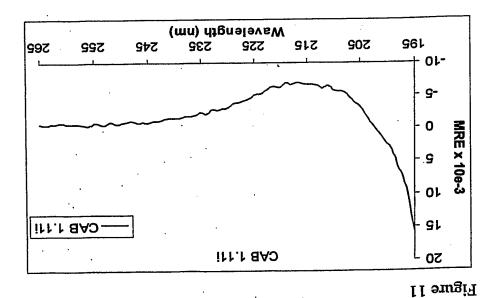
Lane 1: molecular weight standard; Lanes 3-5: unrelated proteins; lane 6: CAB1.11i.

Figure 9



900





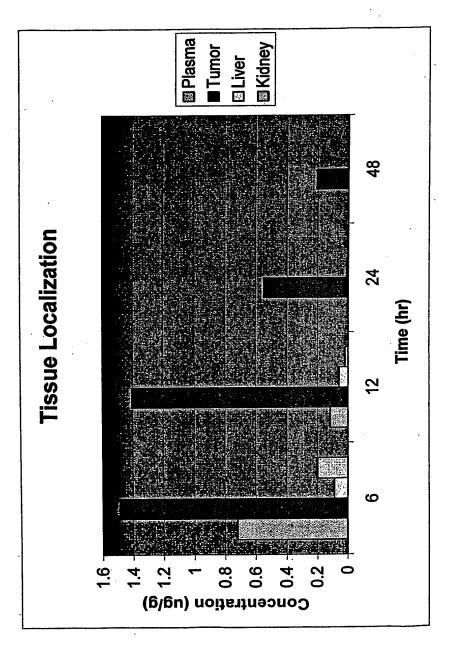


Figure 12

Ratio of Tumor:Blood Concentrations

200

150

50

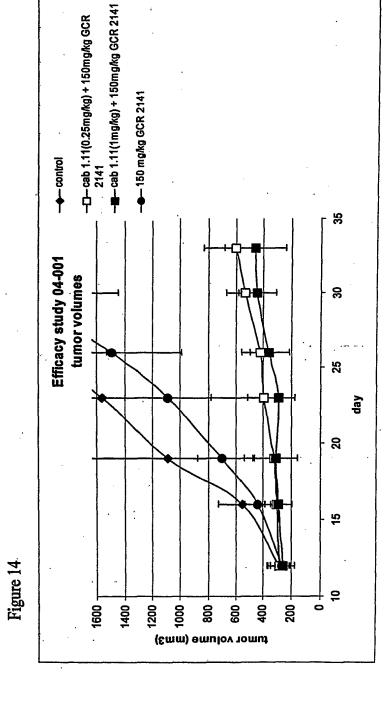
6

12

24

*BLA detected tumor but not in blood.

igure 1.



(SESTION OF SECTION OF	MEYA	Sample 19. See	
<u>CI0000000255</u>	DF5	FR00005C7B	Adenocarcinoma of lung
<u>CIO000005496</u>	E.	ER5B337447	Adenosarsinoma of litrig
<u>CI0000011577</u>	FF1	FR5B34059F	Adenocarcinoma of lung
<u>G170000000244</u>		FRE0033A78	Aceroic arcinom a ciclific At
Cl0000007518	AF5	FR0001FD15	Carcinoma of lung, squamous cell
<u>epococo8475</u>	AF4	FR65EE0784	Adenocarcinoma of colon, metastatis
<u>CI0000015252</u>	FF2	FR5B342166	Adenocarcinoma of colon

32001

(sase Djagno sis	TESUEO (Onclinistra o la multira de la multi	H	20	BENTANTEL.
Adenocarcinoma of lung Grade: AJCC G3: Poorly differentiated Stage: IIIA	Lung/Lung	<u>4X</u>	<u>20X</u>	Immunoger
Adenocarcinome of lune Grade: AJCG G3: Poody differentiated Stage: INE	Lune/Lute		K	
Adenocarcinoma of lung Grade: AJCC G2: Moderately differentiated Stage: IIIA	Lung/Lung	<u>4X</u>	<u>20X</u>	
Adenocarcinoma of Jurg	Lung/Lung.	4	<u> 208.</u>	
Carcinoma of lung, squamous cell Grade: AJCC G3: Poorly differentiated Stage: IIIA	Lung/Lung	4X	<u>20X</u>	
Adenocarcinema of colon, metastatic Grade: Not Reported Stage: IV	E olon/Liver		<u>26×</u>	institute.
Adenocarcinoma of colon Grade: AJCC G3: Poorly differentiated Stage: IIIB	Cecum/Cecum	<u>4×</u>	<u>20X</u>	

FIG. 15-12

luman Gytokeratin AE1/AE3	CAB/GCR3708 (0:2ug/mh	SOADICORES
ncity: Tumor(100%, Variable to 3+ Cyto) Necrosis(Variable to 3+ EC) Specificity: High 20x SF00029758	Immunogencity: Turnor(100%, Variable to 3+ Cyto) Mixed inflammatory cells(Variable to 1+ Cyto) Specificity: High 4x 20x SF00029756	Immunogencity: Tumor(16 Mixed inflammatory cel Necrosis(Varia Specifici 4x
	Immunogenety: Turnor(45%, Variable to 3 + Cyto) Initra-alveolar macropfrages (Variable to 3 + Cyto) Mixed inflammatory collist/variable to 3 + Cyto) Specificity-High 24x SF0002875B	Immunosencile Turrent Intra-alveola magrosia Miceolinjammatory on Spenie 43
	Immunogencity: Tumor(100%, 2+ Cyto) Cellular stroma(1+ Cyto) Chronic inflammatory cells(Variable to 1+ Cyto) Specificity: High 4x SF0002977F	Immunogencity: Tur Cellular stroi Chronic inflammatory ce Specifici 4x SF000
	Immungerucing Ternor(25x, Variable to 6± Cyro) Cellular Stromar(Variable to 2± Eyro) Necresis(Variable to 2± Eyro) Intra-alverdatmerrophages (Variable to 2± Eyro) Specificity Hung: 1x SF 0002978B*: 3322	ingruncoencity: Turney Cellular strange Serricises Intra-alvesia marche Spetar
	immunogencity: Tumor(100%, 3+ Cyto) Fibrotic stroma(1+ Cyto) Necrosis(Variable to 3+ EC) Specificity: High 4x 20x SF0002975F	Immunogencity: Tur Fibrotic stroi Necrosis(Varia Specifici <u>4x</u> <u>SF000</u>
agenety: Lumor (98%, Yanable to 48. Mem, Vanable to 34 Cyte) role stroma (Vanable to 14 Cyte) mai liver parently ma(2+ Cyte) Necrosis (Vanable to 64 EG) Specificity: Hight SECOUSTICATE SECOUS	Immulipaenaty Fumor(98%, Variable to 3+ Main Variable to 3+ Cytoffs Entrolle Stroma(Variable to 4± Cyto) Normal liver parenchymia (1+ Cyto) Necrosis (Variable to 3+ EC) Specificity Hights 4x SF 00029768 Journal liver parenchyma shows positive statung (1+)	Immunoeeelite Transition of the American Service Servi
· ·	Immunogencity: Turnor(65%, Variable to 3+ Mem, Variable to 3+ Cyto) Cellular stroma(1+ Cyto) Normal muscle(Variable to 2+ Cyto) Specificity: High 4x SF00029783	immunogencity: Tumc Mem,Variabli Cellular stroi Normal muscle(Va Specifici 4x

F16. 16- C

176(0:20a/mil)	GAB/GCR67/98 (0/21/6/ml)	GAD/GGR88881041960
00%, Variable to 3+ Cyto) Ils(Variable to 3+ Cyto) able to 2+ EC) ity: High 20x	Immunogencity: Tumor(100%, Variable to 3+ Cyto) Mixed inflammatory cells(Variable to 1+ Cyto) Specificity: High 4x 20x SF00029753	Immunogencity: Tumor(100%, Variable Mixed Inflammatory cells(Variable to Specificity: High 4x 20x SF00029754
KNG Warrable to 31: 0 yley pes (Variable to 21: 0 yley) pes (Variable to 21: 0 yley) per Variable to 21: 0 yley high beautiful to 21	immunogenchy Tumoti 10% Yariahle to 2 + Cylo) infra-alveolar macrophages (Variable to 2 + Cylo) Mixedinflemmatery cells (Variable to 2 + Cylo) Specificity High:	mmunogenery funor(10% Verico) Interalve blas macrophage SN agast Machinian materype Is Normale Specificity High 455-6682975A
mor(100%, 2+ Cyto) ma(1+ Cyto) ells(Variable to 1+ Cyto) ity: High 20x	Immunogendty: Tumor(100%, 2+'Cyto) Cellular stroma(1+ Cyto) Chronic inflammatory cells(Variable to 1+ Cyto) Specificity: High 4x SF0002977D	Immunogencity: Tumor(100%, 2+ Cellular stroma(1+ Cyto) Chronic inflammatory cells(Variable to Specificity: High 4x 20x SF0002977E
ESC. Variable to Str. (Vie) anable in 24 c viola alle to 24 EE 14 ass (Variable to 25 viola is) Highes 20788	Immunogeachy, rumor Cav, i Vanadie ad dt Gulbre Cellular Stomat Vanable (d. 1916). Teoretis Vanable (d. 1916). Teoretis Vanable (d. 1916). Intra-liveolarimacrophages Vanableiru. H. Ovio. Specificity High: 43. Specificity High: SE08029780	Tealmar suoma (Eliable la Vel
Tior(100%, 3+ Cyto) ma(1+ Cyto) able to 3+ EC) lty: High 20x	Immunogencity: Tumor(100%, 3+ Cyto) Fibrotic stroma(1+ Cyto) Necrosis(Variable to 3+ EC) Specificity: High 4x 20x SF0002975D	Immunogencity: Tumor(100%, 3+ Fibrotic stroma(1+ Cyto) Necrosis(Variable to 3+ EC) Specificity: High 4x 20x SF0002975E
n (38%, Variable to six #e# efficies Experiments of the control of	immunogencivic fumor (95%). Variable for the Mem Venible to 4" Cyto) is specific stromat Variable to 5" Cyto No. 2" Normal Tyer parenchymat 1" Cyto). Necrosist Variable to 3" ECX. Specificity Eldit. 4.2.2.2.3.3.3.4.3.4.4.3.4.5.5.5.5.3.3.3.3.3.4.3.3.4.3.3.4.3.3.4.3.3.4.3.3.4.3.3.4.3.3.4.3.3.4.3.3.4.3.3.4.3.3.4.3	Immunosencity surmines and Memoralishe (colors) Fibroic Shomatyanable (colors) Fibroic Shomatyanable (colors) Nemative systemety many Colors (colors) Specificity slight Specificity slight Specificity slight Memoralive specific
x(85%, Variable to 3+ e to 3+ Cyto) ma(1+ Cyto) ariable to 2+ Cyto) ity: High 20x	Immunogencity: Tumor(95%, Variable to 3+ Mem, Variable to 3+ Cyto) Cellular stroma(1+ Cyto) Normal muscle(Variable to 2+ Cyto) Specificity: High 4x 20x SF00029781	Immunogencity: Tumor(95%, Variab Mem, Variable to 3+ Cyto) Cellular stroma(1+ Cyto) Normal muscle(Variable to 2+ C Specificity: High 4x SF00029782
	15-D	

ril)	Notanijodyconiol(Predibled)
to 3+ Cyto) 1+ Cyto)	immunogencity: N/A Specificity: Unknown
	<u>SF00029755</u>
gs + Cyte) 12 + Cyte) 2+ Cyte)	
Cyto)	Annual Control of the
, 1+ Cyto)	
oca+ Cyro) yco) 12 Cyrol	
Cyto)	
ie to 33 viol (to) tainlog (14)	imnunogericty NA Spedicity Unknown.
He to 3+	
yto)	·
	F16 15 E

<u>Ciboeoo17970</u>	951	FR65EE7B3D	Adenocarcinoma of colon
<u>C10000010013</u>	AF2	FR00028F2E	Adenocarcinoma of pancreas, metastatic
<u>©10000009654</u>	AF1	FR0002B111	Adenocaroma of panereas, ductal
<u>C10000008690</u>	CF4	FR00027B0E	Adenocarcinoma of pancreas, ductal
<u>CIDDD0G07678</u>		FR0002575B	Adenocarcinoma of pancreas, duotal
<u>C10000009736</u>	AF2	FR0002BAB4	Adenocarcinoma of pancreas, ductal

FIG. 15-F

	· ·	1	•
Adenocarcinoma of colon Grade AJCC G2: Moderately differentiated Stage NIC	Colon/colon:	# 20X	
Adenocarcinoma of pancreas, metastatic Grade: Not Reported Stage: IV	Pancreas/Omentum	<u>4X 20X</u>	Immu Fibros <u>4x</u>
Adenecarcinema of pancreas, ductal Grade: AJCC G2 Moderately dimerentiated Stage: IIB	Pancieas/Pancieas sta	<u>4X</u> 20X	
Adenocarcinoma of pancreas, ductal Grade: AJCC G1: Well differentiated Stage: IIA	Pancreas/Pancreas	<u>4X</u> <u>20X</u>	
Adenocarcinema of pancreas distall Grade AJCC G2 Moderately differentiated Stage III	Pancreas/Pancreas		
Adenocarcinoma of pancreas, ductal Grade: AJCC G2: Moderately differentiated Stage: IIB	Pancreas/Pancreas	<u>4X</u> <u>20X</u>	

FIG.
15-G

	Immunogendity: Turnor(100%, 3+ Cyne) Cellular stroma(1) Cyne Necrosis(Vanable to 3+ EC) Specifich's High 203 SE00029787	Immunogenetite Tur Gellular stie Necresis (Vara Specific 4x
inogencity: Tumor(100%, 3+ Cyto) adipose tissue(Variable to 1+ Cyto) Specificity: High 20x SF0002977C	Immunogencity: Tumor(100%, 3+ Cyto) Fibroadipose tissue(Variable to 2+ Cyto) Specificity: High 4x 20x SF0002977A	Immuriogencity: Tur Fibroadipose tissue(Specifici 4x <u>SF000.</u>
	Immunogench/ Tumor(180%, 3+ Cyto) Desmoplaste strome(Variable to 2+ Cyto) Specificity: Highl: +: 20x: SF000297771	Immunogenciis: Tur Desmoplastic strane Spesiic 4x
	Immunogendty: Tumor(100%, 3+ Cyto) Myxold stroma(Variable to 2+ Cyto) Specificity: High 4x 20x SF0002976D	Immunogencity: Tur Myxold stroma(Va Specifici <u>4x</u> <u>SF000.</u>
	Immunegeneriy, Turnor(85x; Variable to 3+ Syte) Gellular stroma(Variable to 1+ Cyte) Gluroric pancrealitis(Variable to 1+ Cyte) Specificity: Highe 3F000297634.	Immunogencity Turnsett Calible stroma & Chronic pancreaths \$ 50 person \$ 55 p
	Immunogencity: Tumor(100%, 3+ Cyto) Chronic pancreatitis(Variable to 2+ Cyto) Fibrotic stroma(Variable to 2+ Cyto) Specificity: High 4x 20x SF00029775	Immunogencity: Tur Chronic pancreatitis(Fibrotic stroma(Va Specifici 4x SF000

FIG.

15-H

Tior(180%; 3+ Cyto) ma(1+ Cyto) sole to 5+ ES1 iv: High: 20% [29788]	immunogencity: Tumor(100%; 3+ 5 /le) Callular stroma(1+ 5 /lo) Necrosis(Variable to 3+EG) Specificity: High 20x SF00029785	Immunogeneth/ Tumorf100%; \$4. Cellular stroma(1+) Cyrigh Necrosis (Variable to 3+ ES) Specificity: Highrs 201-1 SECOU29786
mor(100%, 3+ Cyto) (Variable to 2+ Cyto) ity: High 20x 2977B	Immunogencity: Tumor(100%, 3+ Cyto) Fibroadipose tissue(Variable to 2+ Cyto) Specificity: High 4x 20x SF00029777	Immunogencity: Tumor(100%, 3+ Fibroadipose tissue(Variable to 2+ Specificity: High 4x 20x SF00029778
nor(190%; 8+ Cyto) (Variable to 2+ Cyto) livi High	Immunecencity:Tumor(100%, 3+ Cyla) Desmoplastic stromat/ anable to 2= Cyto) Specificity: Highls 2x 20x SE00029776	immunogenciy: Tumor(100%, 6) Desmoplastic stroma(Vanable in 1) Specificity: Figit 2 2 SE0002976F
mor(100%, 3+ Cyto) ariable to 2+ Cyto) ity: High 20x 2976E	Immunogencity: Tumor(100%, 3+ Cyto) Myxold stroma(Variable to 2+ Cyto) Specificity: High 4x 20x SF0002976B	Immunogencity: Tumor(100%, 3+ Myxoid stroma(Variable to 2+ C; Specificity: High <u>4x</u> <u>20x</u> <u>SF0002976C</u>
isw. Variable lest Sylosanable to 1+ Cylo). (variable to 1+ Cylo). (immunocencity:Tumor(85%; Vanable to 3+ Cyto): Cellplar stroma(Vanable to 14 Cyto): Chronic pancreatitis(Vanable to 1+ Cyto): Specificity: High: 20x SFG0029761	immunogendity-Lumor(85%, Variable) Cellular stroma (Vanable to 18 Chronic pancreallus Vanable to 18 Specificity-Filip 20 SF00029762
mor(100%, 3+ Cyto) (Variable to 2+ Cyto) ariable to 2+ Cyto) ity: High 20x	Immunogencity: Tumor(100%, 3+ Cyto) Chronic pancreatitis(Variable to 1+ Cyto) Fibrotic stroma(Variable to 1+ Cyto) Specificity: High 4x 20x SF00029773	immunogencity: Tumor(100%, 3+ Chronic pancreatitis(Variable to 2+ Fibrotic stroma(Variable to 2+ C Specificity: High 4x 20x SF00029774

F16.
15- I

F1G.	(≱	
	Cyto) Cyto)	Immunogencity: N/A Specificity: N/A
		<u>SF00029779</u>
	<u>වී ලි</u>	
	Cyto)	
	Cyto) yto)	ስለተር ነው መስመር መመር መስመር መስመር መስመር መስመር መስመር መስመር
	1996 1996 1996 1996 1996 1996 1996 1996	
	Cyto) Cyto) yto)	

Eliminated From Plasma and Retained in Tumor to At P91 5.1 CAB 1.11.

Least 96 hr

Plasma and tumor GCR-8886 concentration-time profiles (log-linear scale)

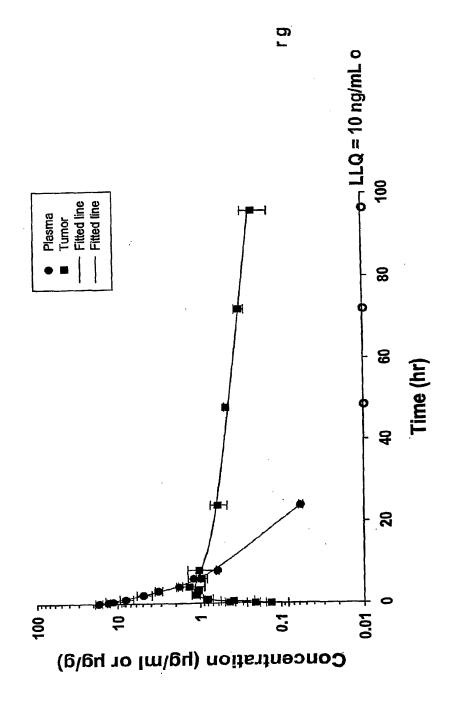
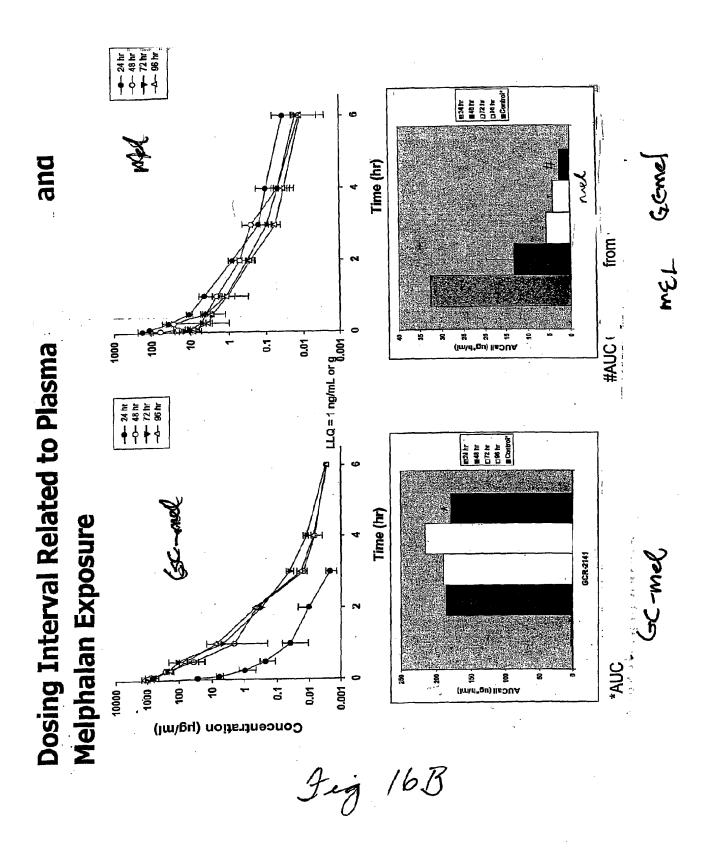
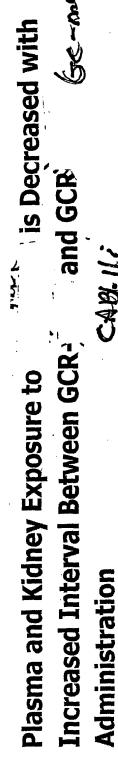
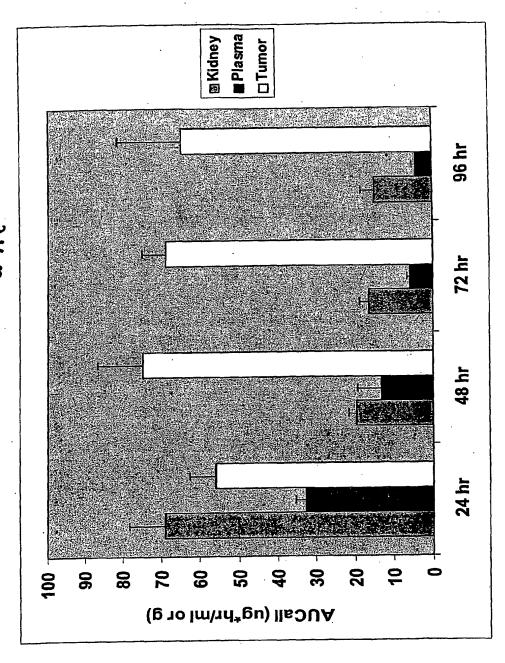


Fig. 16A

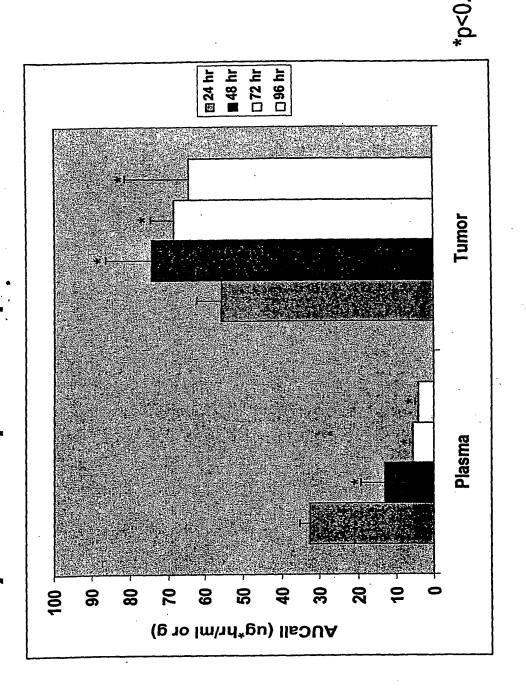






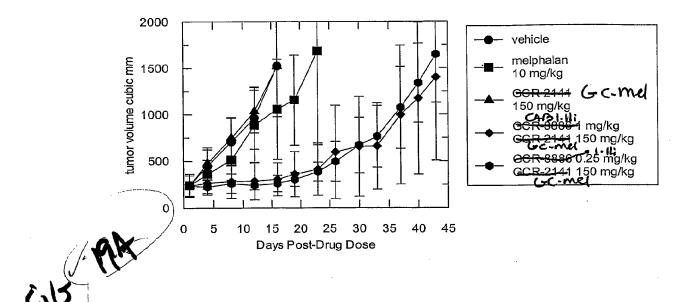
3 mg 17

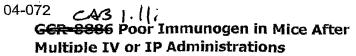
Efficacious Tumor Melphalan Exposures Achieved at Each Time Interval While Systemic Melphalan Exposure Decreased

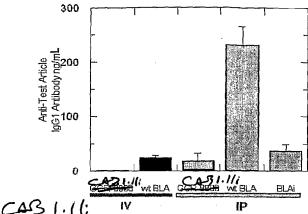


Efficacy demonstrated at 24 hr interval in TLS174T xenograft mouse

model





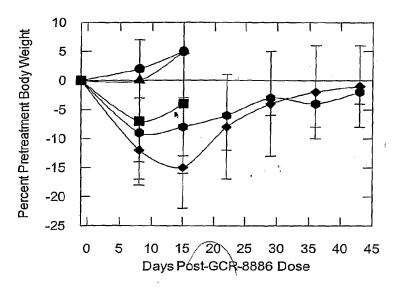


*GER-6866 weakly immunogenic after multiple IP doses in alum- similar to BLAi

Confidential

Fi 6 20

04-066 completed



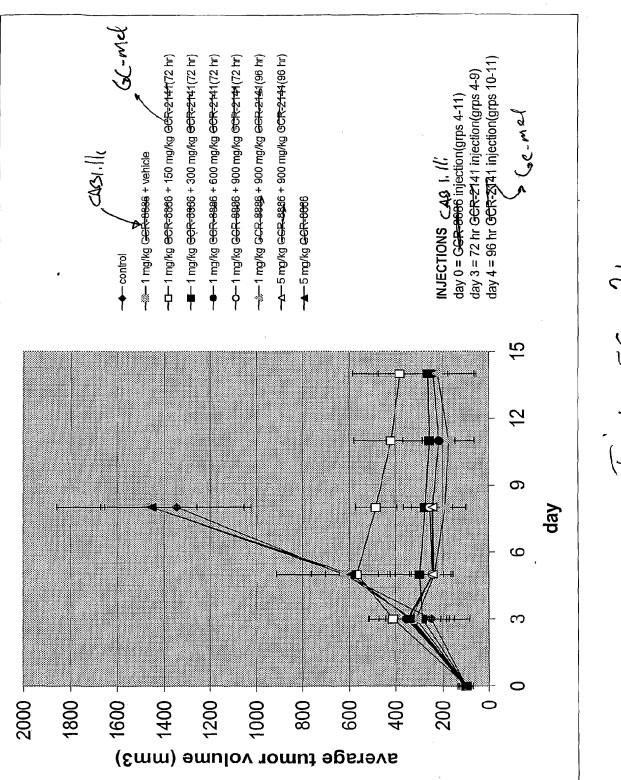
→ Vehicle

- Melphalan
10 mg/kg

- GCR 2141
150 mg/kg

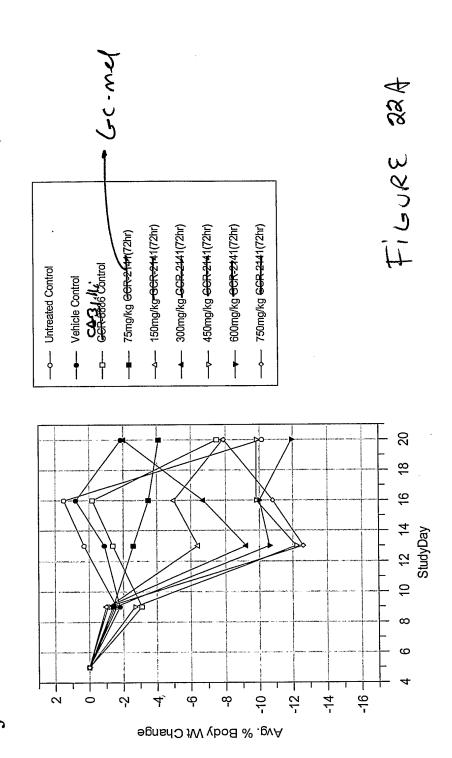
- GCR 8886
0.25 mg/kg
GCR 2141
150 mg/kg
- GCR 8886
1.0 mg/kg
GCR 2141
150 mg/kg
GCR 2141
150 mg/kg
GCR 2141
150 mg/kg
GCR 2141
150 mg/kg

FIG 19B

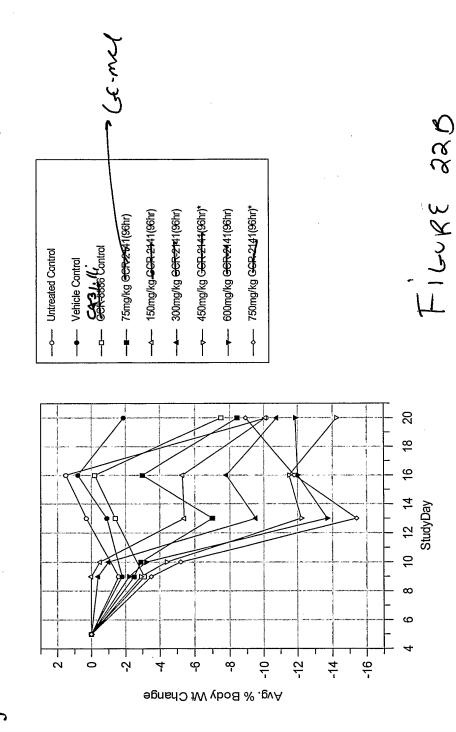


F16-116 21

(5C - m/e) 04-105 — Avg. % Body Wt loss — GCR-2141 injection 72 hrs (Study Day 9) post GCR-8886 injection

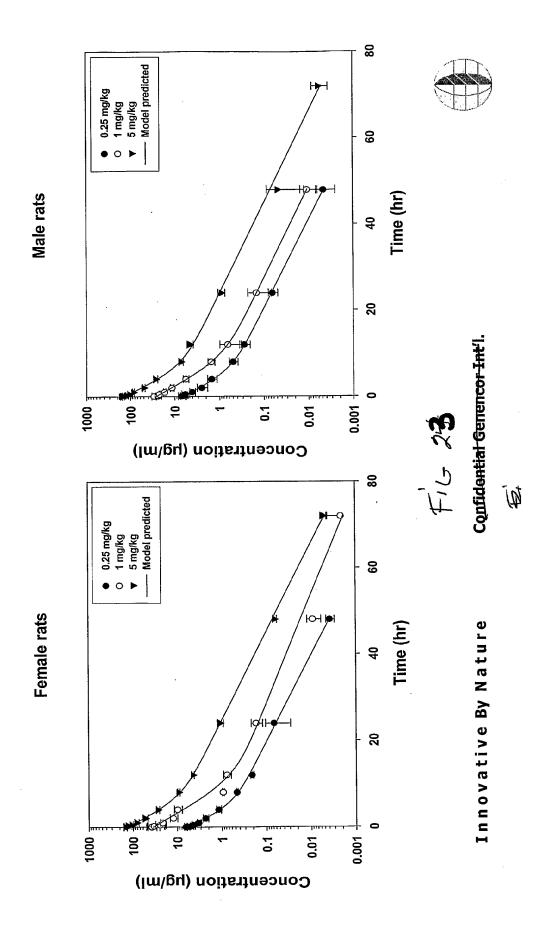


04-105 - Avg. % Body Wt loss - GCR-2141 injection 96 hrs (Study Day 10) post GCR-8886 C43 1:11/ injection



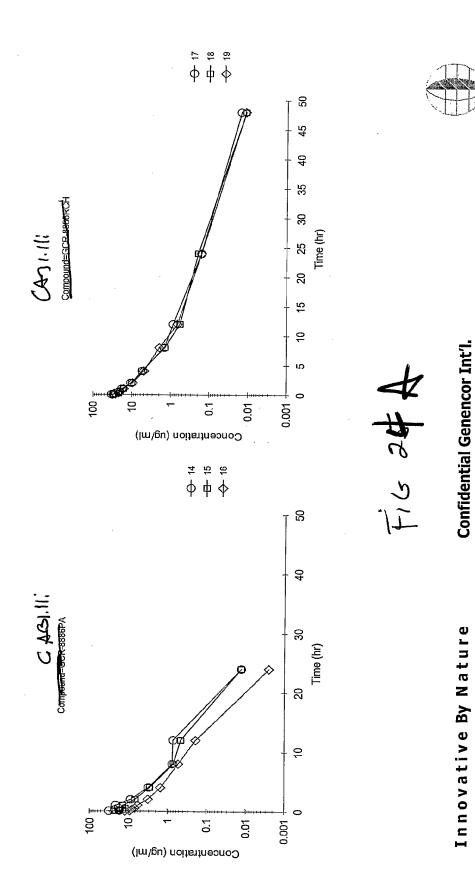
८क्8।स् Plasma GCR-8886 concentration-time profile in rats

Results

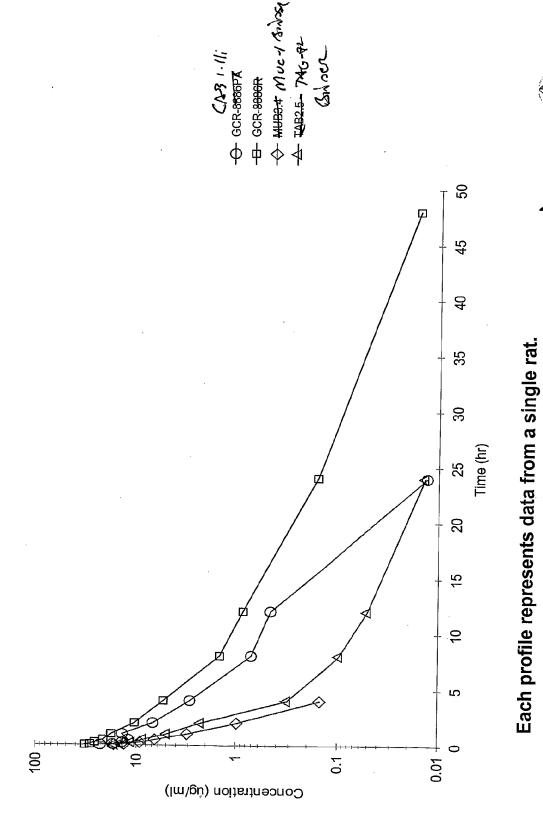


Plasma GCR-8886 concentration-time profiles in rats

Results



Plasma concentration-time profiles in rats Results



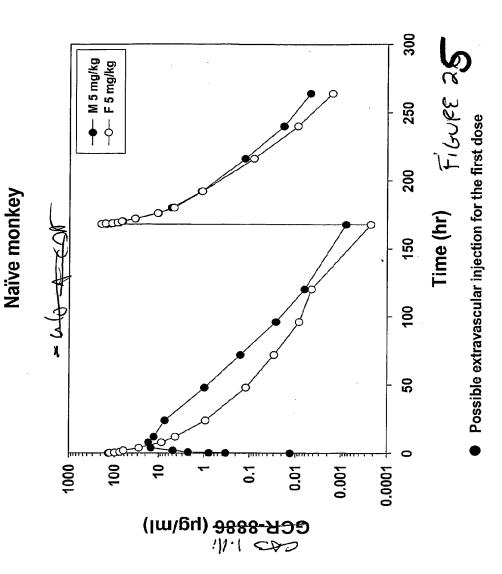
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GCR-8886 concentration-time profiles following 2 weekly doses

Results



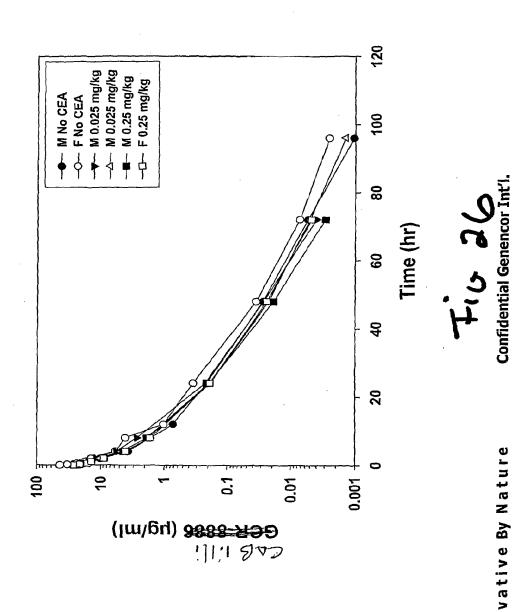
Confidential Genencor Int'l.

Innovative By Nature

|-||-| | 9886 PK parameter estimates with or without CEA coadministration

Results

CA(\$ 1.11; GCR=8886 (1 mg/kg)



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